



results of BLAST

BLASTN 2.2.12 [Aug-07-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1132600206-2671-153796666945.BLASTQ4

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,579,719 sequences; 15,994,705,008 total letters

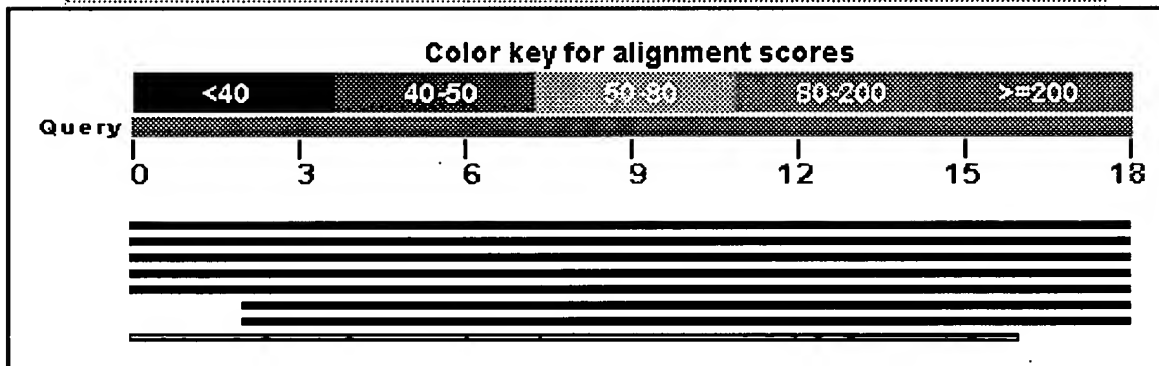
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=

(18 letters)

Distribution of 8 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Sequences producing significant alignments:		Score (Bits)	E Value
qi 33390917 qb AE017171.1 	Staphylococcus aureus plasmid pLW043,	<u>36.2</u>	0.41
qi 21886737 qb AF516335.1 	Enterococcus faecium plasmid pUW78...	<u>36.2</u>	0.41
qi 155036 qb M97297.1 TRNVAN	Enterococcus faecium transposon ...	<u>36.2</u>	0.41
qi 43335 emb X56895.1 EFPVANAG	E.faecium plasmid pIP816 vanA gen	<u>36.2</u>	0.41
qi 57790303 qb AY754011.1 	Enterococcus faecium vancomycin re...	<u>36.2</u>	0.41
qi 12666232 emb AL161898.17 	Human DNA sequence from clone RP...	<u>32.2</u>	6.4
qi 2370068 emb Z92540.1 HS179115A	Human DNA sequence from clo...	<u>32.2</u>	6.4
qi 479085 emb X79049.1 OTPDVANA2	O.turbata Plasmid DNA for vanco	<u>32.2</u>	6.4

Alignments

Get selected sequences

Select all

Deselect all

> ☐ [gi|33390917|gb|AE017171.1|](#) ☒ Staphylococcus aureus plasmid pLW043, complete sequence
Length=57889

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||||
Sbjct 34773  CCGGTGGCAGCTACGTTT 34790
```

> ☐ [gi|21886737|gb|AF516335.1|](#) ☒ Enterococcus faecium plasmid pUW786 multiple antibiotic
gene cluster, complete sequence
Length=17510

Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||||
Sbjct 4222   CCGGTGGCAGCTACGTTT 4239
```

> ☐ [gi|155036|gb|M97297.1|TRNVAN](#) ☒ Enterococcus faecium transposon Tn1546 transposase
vanR (vanR), vanS (vanS), vanH (vanH), vanA (vanA), vanX (vanX),
vanY (vanY), and teicoplanin resistance protein (vanZ)
genes, complete cds
Length=10851


Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||||
Sbjct 7453   CCGGTGGCAGCTACGTTT 7470
```

> ☐ [gi|43335|emb|X56895.1|EFPVANAG](#) E. faecium plasmid pIP816 vanA gene for VANA ligase
Length=1768



Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 1      CCGGTGGCAGCTACGTTT 18
             |||||
Sbjct 851    CCGGTGGCAGCTACGTTT 868
```

>  [gi|57790303|gb|AY754011.1|](#) Enterococcus faecium vancomycin resistance protein A
partial cds
Length=614



Score = 36.2 bits (18), Expect = 0.41
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGTTT 18
|||||
Sbjct 241 CCGGTGGCAGCTACGTTT 258

>  [gi|12666232|emb|AL161898.17|](#)  Human DNA sequence from clone RP11-270H22 on chromosome
sequence
Length=122839


Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 GGTGGCAGCTACGTTT 18
|||||
Sbjct 23455 GGTGGCAGCTACGTTT 23440

>  [gi|2370068|emb|Z92540.1|HS179I15A](#)  Human DNA sequence from clone RP1-179I15 on
a novel gene, a mitochondrial import receptor TOM22 pseudogene,
the 5' end of the KL gene for klotho, ESTs, STSs
and a CpG island, complete sequence
Length=146810

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 GGTGGCAGCTACGTTT 18
|||||
Sbjct 115256 GGTGGCAGCTACGTTT 115241

>  [gi|479085|emb|X79049.1|OTPDVANA2](#) O.turbata Plasmid DNA for vancomycin resistance
Length=786

Score = 32.2 bits (16), Expect = 6.4
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 CCGGTGGCAGCTACGT 16
|||||
Sbjct 345 CCGGTGGCAGCTACGT 360

Get selected sequences

Select all

Deselect all

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental

samples or phase 0, 1 or 2 HTGS sequences)
Posted date: Nov 20, 2005 2:03 AM
Number of letters in database: -1,185,164,172
Number of sequences in database: 3,579,719
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 3579719
Number of Hits to DB: 281356
Number of extensions: 8869
Number of successful extensions: 8869
Number of sequences better than 10: 2
Number of HSP's better than 10 without gapping: 2
Number of HSP's gapped: 8869
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10: 8867
Length of query: 18
Length of database: 15994705008
Length adjustment: 16
Effective length of query: 2
Effective length of database: 15937429504
Effective search space: 31874859008
Effective search space used: 31874859008
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 11 (22.3 bits)
S2: 16 (32.2 bits)